

#4

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 101532,153  
Source: PCT  
Date Processed by STIC: 4-28-05

***ENTERED***



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/532,153

DATE: 04/28/2005  
TIME: 16:26:58

Input Set : A:\Seq Listing.ST25.txt  
Output Set: N:\CRF4\04272005\J532153.raw

3 <110> APPLICANT: Evolutionary Genomics LLC  
 5 <120> TITLE OF INVENTION: Development of Therapeutics for the Treatment of  
 6 Endotoxin-Mediated Diseases  
 8 <130> FILE REFERENCE: GENO200.3.1  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/532,153  
 C--> 10 <141> CURRENT FILING DATE: 2005-04-20  
 10 <150> PRIOR APPLICATION NUMBER: 10/100,422  
 11 <151> PRIOR FILING DATE: 2002-03-18  
 13 <160> NUMBER OF SEQ ID NOS: 40  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 2427  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Pan troglodytes  
 22 <400> SEQUENCE: 1  
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 25 ctccccttct caaccaagaa cctggacctg agctttaatc ccctgaggca ttttaggcagc 120  
 27 tatacgcttc tcagttccc agaaactgcag gtgctggatt tatccaggtg tgaatccag 180  
 29 acaattgaag atggggcata tcagagccta agccacctct ccaccttaat attgacagga 240  
 31 aaccatcc agagtttagc cctgggagcc ttttctggac tatcaagttt acagaagctg 300  
 33 gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctaaaaact 360  
 35 ttgaaaagaac ttaatgtggc tcacaatctt atccaatctt tcaaattacc tgagtatttt 420  
 37 tctaattctga ccaatctaga gcacttggac ctttccagca acaagattca aagtattttat 480  
 39 tgcacagact tgcgggttct acatcaaatg cccctactca atctctctt agacctgtcc 540  
 41 ctgaacccta tgaactttat ccaaccaggc gcattaaag aaatttaggt tcataagctg 600  
 43 actttgagaa ataattttga tagtttaat gtaataaaaa cttgtattca aggtctggct 660  
 45 gttttagaag tccatcggtt ggttctggga gaatttagaa atgaaggaaa cttggaaaag 720  
 47 tttgacaaat ctgctctaga gggcctgtgc aatttgacca ttgaagaatt ccgattagca 780  
 49 tacttagact actaccccgta tgatatttt gacttattta attgtttgac aaatgtttct 840  
 51 tcattttccc tggtagtgt gacttattaa agcgtaaaag acttttctta taatttcgga 900  
 53 tggcaacatt tagaatttagt taactgtaaa ttggacagt ttcccacatt gaaactcaaa 960  
 55 tctctcaaaa ggcttacttt cacttccaaac aaaggggta atgtttttc agaagttgat 1020  
 57 ctaccaagcc ttgagttct agatctcagt agaaatggct tgagttcaa aggttgcgt 1080  
 59 tctcaaagtg attttggac aaccagccta aagtatttag atctgagctt caatgggttt 1140  
 61 attaccatga gttcaaactt ctgggctta gaacaactag aacatctgga tttccagcat 1200  
 63 tccaaattga aacaaatggag tgagtttca gtatttctat cactcagaaa cctcatttac 1260  
 65 cttgacattt ctcatactca caccagagtt gcttcaatg gcatcttcaa tggcttgc 1320  
 67 agtctcgaag tcttggaaat ggctggcaat tctttccagg aaaacttctt tccagatatc 1380  
 69 ttcacagagc tgagaaactt gaccccttc gaccccttc achtgtcaact ggagcagttg 1440  
 71 tctccaacag catttaactc actctccagt cttcaggtac taaatatggag ccacaacaac 1500  
 73 ttctttcat tggatacggtt tccttataag tgtctgaact ccctccaggt tcttgattac 1560  
 75 agtctcaatc acataatgac ttccaaaaaaaaa caggaactac agcattttcc aagttagtcta 1620  
 77 gcttcttaa atcttactca gaatgactt gcttgcattt gtgaacacca aagtttcctg 1680

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79	caatggatca	aggaccagag	gcagctcttg	gtggaagttg	aacgaatgga	atgtgcaaca	1740										
81	ccttcagata	agcagggcat	gcctgtgctg	agtttgaata	tcacctgtca	gatgaataag	1800										
83	accatcattg	gtgtgtcggt	cctcagtgtg	ctttagtat	ctgttgttagc	agttctggc	1860										
85	tataagttct	atttcacct	gatgcttctt	gctggctgca	taaagtatgg	tagaggtgaa	1920										
87	aacatctatg	atgccttgt	tatctactca	agccaggatg	aggactgggt	aaggaatgag	1980										
89	ctagtaaaga	atttagaaga	agggggtgcct	ccatttcagc	tctgccttca	ctacagagac	2040										
91	tttattcccg	gtgtggccat	tgtgccaac	atcatccatg	aaggtttcca	taaaagccga	2100										
93	aaggtgattg	ttgtgggtgc	ccagcacttc	atccagagcc	gctgggtgtat	ctttgaatat	2160										
95	gagattgctc	agacctggca	gtttctgagc	agtcgtgctg	gtatcatctt	cattgtcctg	2220										
97	cagaagggtgg	agaagaccct	gctcaggcgg	caggtggagc	tgtaccgcct	tctcagcagg	2280										
99	aacacttacc	tggagtgggg	ggacagtgtc	ctggggcggc	acatttctg	gagacgactc	2340										
101	agaaaagccc	tgctgatgg	taaatcatgg	aatccagaag	gaacagtggg	tacaggatgc	2400										
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107	<211>	LENGTH:	2427														
108	<212>	TYPE:	DNA														
109	<213>	ORGANISM:	Pan troglodytes														
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113	<221>	NAME/KEY:	CDS														
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119	1				5			10							15		
121	atc	ccc	gac	aac	ctc	ccc	ttc	tca	acc	aag	aac	ctg	gac	ctg	agc	ttt	
122	Ile	Pro	Asp	Asn	Leu	Pro	Phe	Ser	Thr	Lys	Asn	Leu	Asp	Leu	Ser	Phe	
123					20			25				30					
125	aat	ccc	ctg	agg	cat	tta	ggc	agc	tat	agc	ttc	ttc	agt	ttc	cca	gaa	
126	Asn	Pro	Leu	Arg	His	Leu	Gly	Ser	Tyr	Ser	Phe	Phe	Ser	Phe	Pro	Glu	
127					35			40				45					
129	ctg	cag	gtg	ctg	gat	tta	tcc	agg	tgt	gaa	atc	cag	aca	att	gaa	gat	
130	Leu	Gln	Val	Leu	Asp	Leu	Ser	Arg	Cys	Glu	Ile	Gln	Thr	Ile	Glu	Asp	
131					50			55			60						
133	ggg	gca	tat	cag	agc	cta	agc	cac	ctc	tcc	acc	tta	ata	ttg	aca	gga	
134	Gly	Ala	Tyr	Gln	Ser	Leu	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Thr	Gly	
135					65			70			75			80			
137	aac	ccc	atc	cag	agt	tta	gcc	ctg	gga	gcc	ttt	tct	gga	cta	tca	agt	
138	Asn	Pro	Ile	Gln	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Ser	Gly	Leu	Ser	Ser	
139					85			90			95						
141	tta	cag	aag	ctg	gtg	gct	gtg	gag	aca	aat	cta	gca	tct	cta	gag	aac	
142	Leu	Gln	Lys	Leu	Val	Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Leu	Glu	Asn	
143					100			105			110						
145	ttc	ccc	att	gga	cat	ctc	aaa	act	ttg	aaa	gaa	ctt	aat	gtg	gct	cac	
146	Phe	Pro	Ile	Gly	His	Leu	Lys	Thr	Leu	Lys	Glu	Leu	Asn	Val	Ala	His	
147					115			120			125						
149	aat	ctt	atc	caa	tct	ttc	aaa	tta	cct	gag	tat	ttt	tct	aat	ctg	acc	
150	Asn	Leu	Ile	Gln	Ser	Phe	Lys	Leu	Pro	Glu	Tyr	Phe	Ser	Asn	Leu	Thr	
151					130			135			140						
153	aat	cta	gag	cac	ttg	gac	ctt	tcc	agc	aac	aag	att	caa	agt	att	tat	

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154	Asn	Leu	Glu	His	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Ser	Ile	Tyr	
155	145				150					155					160		
157	tgc	aca	gac	ttg	cg	gtt	cta	cat	caa	atg	ccc	cta	ctc	aat	ctc	tct	528
158	Cys	Thr	Asp	Leu	Arg	Val	Leu	His	Gln	Met	Pro	Leu	Leu	Asn	Leu	Ser	
159					165					170					175		
161	tta	gac	ctg	tcc	ctg	aac	cct	atg	aac	ttt	atc	caa	cca	gg	gca	ttt	576
162	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Met	Asn	Phe	Ile	Gln	Pro	Gly	Ala	Phe	
163					180					185					190		
165	aaa	gaa	att	agg	ctt	cat	aag	ctg	act	ttg	aga	aat	aat	ttt	gat	agt	624
166	Lys	Glu	Ile	Arg	Leu	His	Lys	Leu	Thr	Leu	Arg	Asn	Asn	Phe	Asp	Ser	
167			195					200					205				
169	tta	aat	gta	atg	aaa	act	tgt	att	caa	gg	ctg	gct	gg	tta	gaa	gtc	672
170	Leu	Asn	Val	Met	Lys	Thr	Cys	Ile	Gln	Gly	Leu	Ala	Gly	Leu	Glu	Val	
171			210					215					220				
173	cat	cgt	ttg	gtt	ctg	gga	gaa	ttt	aga	aat	gaa	gga	aa	ttg	gaa	aag	720
174	His	Arg	Leu	Val	Leu	Gly	Glu	Phe	Arg	Asn	Glu	Gly	Asn	Leu	Glu	Lys	
175			225			230				235					240		
177	ttt	gac	aaa	tct	gct	cta	gag	ggc	ctg	tgc	aat	ttg	acc	att	gaa	gaa	768
178	Phe	Asp	Lys	Ser	Ala	Leu	Glu	Gly	Leu	Cys	Asn	Leu	Thr	Ile	Glu	Glu	
179					245				250					255			
181	tcc	cga	tta	gca	tac	tta	gac	tac	tac	ctc	gat	gat	att	att	gac	tta	816
182	Phe	Arg	Leu	Ala	Tyr	Leu	Asp	Tyr	Tyr	Leu	Asp	Asp	Ile	Ile	Asp	Leu	
183			260				265						270				
185	ttt	aat	tgt	ttg	aca	aat	gtt	tct	tca	ttt	tcc	ctg	gtg	agt	gtg	act	864
186	Phe	Asn	Cys	Leu	Thr	Asn	Val	Ser	Ser	Phe	Ser	Leu	Val	Ser	Val	Thr	
187			275				280					285					
189	att	aaa	agc	gta	aaa	gac	ttt	tct	tat	aat	ttc	gga	tgg	caa	cat	tta	912
190	Ile	Lys	Ser	Val	Lys	Asp	Phe	Ser	Tyr	Asn	Phe	Gly	Trp	Gln	His	Leu	
191			290				295					300					
193	gaa	tta	gtt	aac	tgt	aaa	ttt	gga	cag	ttt	ccc	aca	ttg	aaa	ctc	aaa	960
194	Glu	Leu	Val	Asn	Cys	Lys	Phe	Gly	Gln	Phe	Pro	Thr	Leu	Lys	Leu	Lys	
195			305			310				315					320		
197	tct	ctc	aaa	agg	ctt	act	tcc	act	tcc	aac	aaa	gg	gg	aat	gct	ttt	1008
198	Ser	Leu	Lys	Arg	Leu	Thr	Phe	Thr	Ser	Asn	Lys	Gly	Gly	Asn	Ala	Phe	
199					325				330					335			
201	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	ttt	cta	gat	ctc	agt	aga	aat	1056
202	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	Phe	Leu	Asp	Leu	Ser	Arg	Asn	
203			340				345					350					
205	ggc	ttg	agt	ttc	aaa	gg	tgc	tgt	tct	caa	agt	gat	ttt	ggg	aca	acc	1104
206	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	Gln	Ser	Asp	Phe	Gly	Thr	Thr	
207			355				360					365					
209	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	aat	gg	ttt	att	acc	atg	agt	1152
210	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Gly	Val	Ile	Thr	Met	Ser	
211			370				375					380					
213	tca	aac	tcc	ttg	ggc	tta	gaa	caa	cta	gaa	cat	ctg	gat	ttc	cag	cat	1200
214	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	Glu	His	Leu	Asp	Phe	Gln	His	
215			385			390				395					400		
217	tcc	aat	ttg	aaa	caa	atg	agt	gag	ttt	tca	gta	ttc	cta	tca	ctc	aga	1248
218	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	

**RAW SEQUENCE LISTING**  
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**Input Set : A:\Seq Listing.ST25.txt**  
**Output Set: N:\CRF4\04272005\J532153.raw**

219	405	410	415	
221 aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc				1296
222 Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe				
223 420	425	430		
225 aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg aaa atg gct				1344
226 Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala				
227 435	440	445		
229 ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc aca gag ctg				1392
230 Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu				
231 450	455	460		
233 aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg gag cag ttg				1440
234 Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu				
235 465	470	475	480	
237 tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta cta aat atg				1488
238 Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met				
239 485	490	495		
241 agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat aag tgt ctg				1536
242 Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu				
243 500	505	510		
245 aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata atg act tcc				1584
246 Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser				
247 515	520	525		
249 aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct ttc tta aat				1632
250 Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn				
251 530	535	540		
253 ctt act cag aat gac ttt gct tgt act tgt gaa cac caa agt ttc ctg				1680
254 Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu				
255 545	550	555	560	
257 caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt gaa cga atg				1728
258 Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met				
259 565	570	575		
261 gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg ctg agt ttg				1776
262 Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu				
263 580	585	590		
265 aat atc acc tgt cag atg aat aag acc atc att ggt gtg tcg gtc ctc				1824
266 Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu				
267 595	600	605		
269 agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat aag ttc tat				1872
270 Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr				
271 610	615	620		
273 ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa				1920
274 Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu				
275 625	630	635	640	
277 aac atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg				1968
278 Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp				
279 645	650	655		
281 gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct cca ttt				2016
282 Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe				
283 660	665	670		

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285 cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct	2064
286 Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala	
287 675 680 685	
289 gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt	2112
290 Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val	
291 690 695 700	
293 gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat	2160
294 Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr	
295 705 710 715 720	
297 gag att gct cag acc tgg cag ttt ctg agc agt cgt gct ggt atc atc	2208
298 Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile	
299 725 730 735	
301 ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cgg cag gtg	2256
302 Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Arg Gln Val	
303 740 745 750	
305 gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gac	2304
306 Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp	
307 755 760 765	
309 agt gtc ctg ggg cg <sup>g</sup> cac atc ttc tgg aga cga ctc aga aaa gcc ctg	2352
310 Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu	
311 770 775 780	
313 ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt aca gga tgc	2400
314 Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys	
315 785 790 795 800	
317 aat tgg cag gaa gca aca tct atc tga	2427
318 Asn Trp Gln Glu Ala Thr Ser Ile	
319 805	
322 <210> SEQ ID NO: 3	
323 <211> LENGTH: 808	
324 <212> TYPE: PRT	
325 <213> ORGANISM: Pan troglodytes	
327 <400> SEQUENCE: 3	
329 Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys	
330 1 5 10 15	
333 Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe	
334 20 25 30	
337 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu	
338 35 40 45	
341 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp	
342 50 55 60	
345 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly	
346 65 70 75 80	
349 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser	
350 85 90 95	
353 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn	
354 100 105 110	
357 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His	
358 115 120 125	
361 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr	

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 198,683  
Seq#:9; Xaa Pos. 198,683  
Seq#:11; Xaa Pos. 635  
Seq#:12; Xaa Pos. 635  
Seq#:17; Xaa Pos. 14,462  
Seq#:18; Xaa Pos. 14,462  
Seq#:23; Xaa Pos. 758  
Seq#:24; Xaa Pos. 758

**VERIFICATION SUMMARY**

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Input Set : A:\Seq Listing.ST25.txt  
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1198 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:8  
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:624  
M:341 Repeated in SeqNo=8  
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:192  
M:341 Repeated in SeqNo=9  
L:1830 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:11  
L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1920  
L:2042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:624  
L:2665 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:17  
L:2665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:48  
M:341 Repeated in SeqNo=17  
L:2886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
M:341 Repeated in SeqNo=18  
L:3885 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23  
L:3885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:2304  
L:4101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:752